

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
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Brazil
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

TITLE
JOURNAL
MEDLINE
COMMENT

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?C=RC5&I2=RC5-GN0281-
240101-021-F02&S=2003-01-23&t4=1)
Seq primer: puc 18 forward
High quality sequence step: 214.
Location/Qualifiers
1..214
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0281"
/dev_stage="Adult"
/note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 67 a 36 c 88 g 23 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0168 Length: 214
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DH: 13 Gaps: 0
US-09-856-070-21 (1-12) x B1054475 (1-214)
Q7 1 GlutathioneMetLeuAcLeuGlnAspTyrCluGlu 12
|||||
Db 56 CAGGAGTTCAGCTGCGGCTGCAGGACTATGAGGAG 91
RESULT 2
B1054475 214 bp mpna linear EST 15 JUN 2001
LOCUS B1054475 RC5-GN0281 610291-012 RC5-GN0281 Homo sapiens cDNA, mRNA sequence
DEFINITION B1054475
ACCESSION B1054475
VERSION B1054475.1 GI:14462005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 214)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zado,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and
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Email: asimpson@ludwig.org.br
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(http://www.ludwig.org.br/scripts/gethtml2.pl?C=RC5-GN0281-
010201-012-H01&S=2001-02-01&t4=1)
Seq primer: puc 18 forward
High quality sequence step: 214.
Location/Qualifiers
1..214
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0281"
/dev_stage="Adult"
/note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
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Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 68 a 36 c 88 g 22 t
ORIGIN

FEATURES
source

Alignment Scores:
Pred. No.: 0.0168 Length: 214
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DH: 13 Gaps: 0
US-09-856-070-21 (1-12) x B1054475 (1-214)
Q7 1 GlutathioneMetLeuAcLeuGlnAspTyrCluGlu 12
|||||
Db 56 CAGGAGTTCAGCTGCGGCTGCAGGACTATGAGGAG 91
RESULT 3
BQ367833/c 215 bp mRNA linear EST 21-MAY-2002
LOCUS BQ367833 RC5-GN0281 150201-013 AC9-GN0281 Homo sapiens cDNA, mRNA sequence
DEFINITION BQ367833
ACCESSION BQ367833
VERSION BQ367833.1 GI:21043334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 215)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zado,M.A., Bordin,S., Costa,F.,
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20202663
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Fax: +55-11-2707001

TITLE
JOURNAL
MEDLINE
COMMENT

US-09-856-070-21 (1-12) x B1054475 (1-214)
Q7 1 GlutathioneMetLeuAcLeuGlnAspTyrCluGlu 12
|||||
Db 56 CAGGAGTTCAGCTGCGGCTGCAGGACTATGAGGAG 91
RESULT 3
BQ367833/c 215 bp mRNA linear EST 21-MAY-2002
LOCUS BQ367833 RC5-GN0281 150201-013 AC9-GN0281 Homo sapiens cDNA, mRNA sequence
DEFINITION BQ367833
ACCESSION BQ367833
VERSION BQ367833.1 GI:21043334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 215)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
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Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
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M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and
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Fax: +55-11-2707001

US-09-856-070-21 (1-12) x AW845219 (1 281)

QY 1 Glut1LeuMeLeuArqLeuClAspTyrCluCl 12
 DB 176 GAGGACTGATGCTGGCGCTCAGGACTATCAGGAG 211

RESULT 8

BI050028/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT

LABORATORY

INSTITUTE

ADDRESS

POSTAL

CODE

TELEPHONE

FAX

EMAIL

PROJECT

URL

SEQ PRIMER

High quality

sequence

stop: 294.

FEATURES

source

location/qualifiers

1..294

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="GN0294"

/dev_stage="Adult"

/note="Organ: placenta, normal; Vector: puc18; Site_1: SmaI"

; Site_2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT

ORIGIN

Alignment Scores:

Prod. No.: 0.0266

Score: 60.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 13

US-09-856-070-21 (1-12) x BI050028 (1 294)

QY 1 Glut1LeuMeLeuArqLeuClAspTyrCluCl 12

DB 213 GAGGACTGATGCTGGCGCTCAGGACTATCAGGAG 178

RESULT 9

BF869430

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT

LABORATORY

INSTITUTE

ADDRESS

POSTAL

CODE

TELEPHONE

FAX

EMAIL

PROJECT

URL

SEQ PRIMER

High quality

sequence

stop: 297.

FEATURES

source

location/qualifiers

1..297

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ET0148"

/dev_stage="Adult"

/note="Organ: lung tumor; Vector: puc18; Site_1: SmaI"

; Site_2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT

ORIGIN

Alignment Scores:

Prod. No.: 0.037

Score: 60.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 12

US-09-856-070-21 (1-12) x BF869430 (1-297)

QY 1 Glut1LeuMeLeuArqLeuClAspTyrCluCl 12

DB 121 GAGGACTGATGCTGGCGCTCAGGACTATCAGGAG 156

RESULT 10

BMB27086

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

CONTACT

LABORATORY

INSTITUTE

ADDRESS

POSTAL

CODE

TELEPHONE

FAX

EMAIL

PROJECT

URL

SEQ PRIMER

High quality

sequence

stop: 297.

FEATURES

source

location/qualifiers

1..297

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ET0148"

/dev_stage="Adult"

/note="Organ: lung tumor; Vector: puc18; Site_1: SmaI"

; Site_2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT

ORIGIN

Alignment Scores:

Prod. No.: 0.037

Score: 60.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 12

US-09-856-070-21 (1-12) x BMB27086 (1-297)

QY 1 Glut1LeuMeLeuArqLeuClAspTyrCluCl 12

DB 121 GAGGACTGATGCTGGCGCTCAGGACTATCAGGAG 156

[illegible]


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source
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/clone="S4SN01-18-012"
/clone_lib="S4SN01"
/sex="M"
/tissue_type="Stomach"
/cell_type="lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pTZ18Rpl; Site_1: EcoRI;
Site_2: NotI; The poly (A) RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deprotected
with tobacco acid pyrophosphatase (TAP). The deprotected
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-saturated mRNA by
priming with di-tailed vector. The di-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT      127 a      83 c      141 q      53 t
ORIGIN
Alignment Scores:
Pred. No.:      0.042      Length:      404
Score:          60.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:             14      Gaps:      0

US-09-856-070-21 (1-12) x HQ300862 (1-413)
QY 1 GluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 12
|||||
Db 273 GAGCAGTCGATGCTGGGCGCTGCAGGACATAGAGGAG 308

RESULT 15
HQ300862/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
SEQUENCE TAGS
JOURNAL
MEDLINE
COMMENT

```

This sequence was derived from the FAPES/LICR Human Cancer Genome project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&l2=MR4-KT0047-160501-003-104&t3=2001-05-16&l4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 413.

FEATURES
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_lib="KT0047"
 /dev_stage="Adult"
 /note="Organ: bladder tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 tissues into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 46 a 156 c 86 g 125 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.0433 Length: 413
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 US-09-856-070-21 (1-12) x HQ300862 (1-413)
 QY 1 GluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 12
 |||||
 Db 189 GAGCAGTCGATGCTGGGCGCTGCAGGACATAGAGGAG 154

Search completed: January 16, 2003, 21:37:07
 Job time : 1588.77 secs